

SEQUENCE LISTING

AP20 Rec'd CEMPTO 23 MAR 2006

<110> Alitalo et al

<120> VEGF-C OR VEGF-D MATERIALS AND METHODS FOR OLIGODENDROCYTES

<130> 28967/39670A

<160> 38

<170> PatentIn version 3.0

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<213> Homo sapiens

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Ile Glu Ser Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr	
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His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Asp Pro Tyr
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Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
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Tyr Pro Ser His Gln Asn Cys Glu Trp Ile Val Tyr Ala Pro Glu Pro
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Asn Gln Lys Ile Val Leu Asn Phe Asn Pro His Phe Glu Ile Glu Lys
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His Asp Cys Lys Tyr Asp Phe Ile Glu Ile Arg Asp Gly Asp Ser Glu
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Ser Ala Asp Leu Leu Gly Lys His Cys Gly Asn Ile Ala Pro Pro Thr
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Gly Ser Glu Asp Cys Ser Lys Asn Phe Thr Ser Pro Asn Gly Thr Ile
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Glu Ser Pro Gly Phe Pro Glu Lys Tyr Pro His Asn Leu Asp Cys Thr
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Phe Thr Ile Leu Ala Lys Pro Lys Met Glu Ile Ile Leu Gln Phe Leu
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Ile Phe Asp Leu Glu His Asp Pro Leu Gln Val Gly Glu Gly Asp Cys
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Lys Tyr Asp Trp Leu Asp Ile Trp Asp Gly Ile Pro His Val Gly Pro
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Leu Ile Gly Lys Tyr Cys Gly Thr Lys Thr Pro Ser Glu Leu Arg Ser
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Ser Thr Gly Ile Leu Ser Leu Thr Phe His Thr Asp Met Ala Val Ala
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Lys Asp Gly Phe Ser Ala Arg Tyr Tyr Leu Val His Gln Glu Pro Leu
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Glu Asn Phe Gln Cys Asn Val Pro Leu Gly Met Glu Ser Gly Arg Ile
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Leu Leu Leu Tyr Cys Thr Cys Ser Tyr Ser Gly Leu Ser Ser Arg Ser
885 890 895

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His Lys Thr Phe Cys His Trp Glu His Asp Ser His Ala Gln Leu Arg
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Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys
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Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu
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Trp Met Val Val Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val
755 760 765

Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu
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Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile
785 790 795 800

Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Thr Asp Leu Asp
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Lys Lys Asn Thr Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly
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Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly
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Asn Val Leu Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met
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Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr
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Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu
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aat cct gaa gat gac aaa gta tac ttt ttc ttc cgt gaa aat gca ata Asn Pro Glu Asp Asp Lys Val Tyr Phe Phe Phe Arg Glu Asn Ala Ile 240 245 250	771
gat gga gaa cac tct gga aaa gct act cac gct aga ata ggt cag ata Asp Gly Glu His Ser Gly Lys Ala Thr His Ala Arg Ile Gly Gln Ile 255 260 265	819
tgc aag aat gac ttt gga ggg cac aga agt ctg gtg aat aaa tgg aca Cys Lys Asn Asp Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr 270 275 280	867
aca ttc ctc aaa gct cgt ctg att tgc tca gtg cca ggt cca aat ggc Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly 285 290 295 300	915
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aaa gat cct aaa aat cca gtt gta tat gga gtg ttt acg act tcc agt Lys Asp Pro Lys Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser 320 325 330	1011
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aga agg gtg ttc ctt ggt cca tat gcc cac agg gat gga ccc aac tat Arg Arg Val Phe Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr 350 355 360	1107

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Gln Trp Val Pro Tyr 370 Gln Gly Arg Val Pro Tyr 375 Pro Arg Pro Gly Thr 380	
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Cys Pro Ser Lys 385 Thr Phe Gly Gly Phe Asp 390 Ser Thr Lys Asp 395 Leu Pro	
gat gat gtt ata acc ttt gca aga agt cat cca gcc atg tac aat cca	1251
Asp Asp Val Ile Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro	
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Val Phe Pro Met Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn	
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Tyr Gln Phe Thr Gln Ile Val Val Asp Arg Val Asp 440 Ala Glu Asp Gly	
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Gln Tyr Asp Val Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys	
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Val Val Ser Ile Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu	
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Leu Glu Glu Met Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met	
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Glu Leu Ser Thr Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly	
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gtt gcc cag ctc cct tta cac cgg tgt gat att tac ggg aaa gcg tgt	1587
Val Ala Gln Leu Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys	
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Ala Glu Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser	
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Ala Cys Ser Arg Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln	
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gat ata aga aat gga gac cca ctg act cac tgt tca gac tta cac cat	1731
Asp Ile Arg Asn Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His	
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Asp Asn His His Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val	
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Glu Asn Ser Ser Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala	
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ctg gtc tat tgg caa ttc cag agg cga aat gaa gag cga aaa gaa gag	1875
Leu Val Tyr Trp Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu	
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 Ile Arg Val Asp Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu
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 Arg Ser Leu Gln Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val
 640 645 650

gaa cat ggg ttc ata caa act ctt ctt aag gta acc ctg gaa gtc att 2019
 Glu His Gly Phe Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile
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gac aca gag cat ttg gaa gaa ctt ctt cat aaa gat gat gat gga gat 2067
 Asp Thr Glu His Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp
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ggc tct aag acc aaa gaa atg tcc aat agc atg aca cct agc cag aag 2115
 Gly Ser Lys Thr Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys
 685 690 695 700

gtc tgg tac aga gac ttc atg cag ctc atc aac cac ccc aat ctc aac 2163
 Val Trp Tyr Arg Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn
 705 710 715

acg atg gat gag ttc tgt gaa caa gtt tgg aaa agg gac cga aaa caa 2211
 Thr Met Asp Glu Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln
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cgt cgg caa agg cca gga cat acc cca ggg aac agt aac aaa tgg aag 2259
 Arg Arg Gln Arg Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys
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cac tta caa gaa aat aag aaa ggt aga aac agg agg acc cac gaa ttt 2307
 His Leu Gln Glu Asn Lys Lys Gly Arg Asn Arg Arg Thr His Glu Phe
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gag agg gca ccc agg agt gtc tga gctgcattac ctctagaaac ctcaaacaag 2361
 Glu Arg Ala Pro Arg Ser Val
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Lys Leu Ser Tyr Lys Glu Met Leu Glu Ser Asn Asn Val Ile Thr Phe
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 Asn Gly Leu Ala Asn Ser Ser Ser Tyr His Thr Phe Leu Leu Asp Glu
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 Glu Arg Ser Arg Leu Tyr Val Gly Ala Lys Asp His Ile Phe Ser Phe
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 Asp Leu Val Asn Ile Lys Asp Phe Gln Lys Ile Val Trp Pro Val Ser
 85 90 95
 Tyr Thr Arg Arg Asp Glu Cys Lys Trp Ala Gly Lys Asp Ile Leu Lys
 100 105 110
 Glu Cys Ala Asn Phe Ile Lys Val Leu Lys Ala Tyr Asn Gln Thr His
 115 120 125
 Leu Tyr Ala Cys Gly Thr Gly Ala Phe His Pro Ile Cys Thr Tyr Ile
 130 135 140
 Glu Ile Gly His His Pro Glu Asp Asn Ile Phe Lys Leu Glu Asn Ser
 145 150 155 160
 His Phe Glu Asn Gly Arg Gly Lys Ser Pro Tyr Asp Pro Lys Leu Leu
 165 170 175
 Thr Ala Ser Leu Leu Ile Asp Gly Glu Leu Tyr Ser Gly Thr Ala Ala
 180 185 190
 Asp Phe Met Gly Arg Asp Phe Ala Ile Phe Arg Thr Leu Gly His His
 195 200 205
 His Pro Ile Arg Thr Glu Gln His Asp Ser Arg Trp Leu Asn Asp Pro
 210 215 220
 Lys Phe Ile Ser Ala His Leu Ile Ser Glu Ser Asp Asn Pro Glu Asp
 225 230 235 240
 Asp Lys Val Tyr Phe Phe Phe Arg Glu Asn Ala Ile Asp Gly Glu His
 245 250 255
 Ser Gly Lys Ala Thr His Ala Arg Ile Gly Gln Ile Cys Lys Asn Asp
 260 265 270
 Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys
 275 280 285

Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly Ile Asp Thr His
 290 295 300

Phe Asp Glu Leu Gln Asp Val Phe Leu Met Asn Phe Lys Asp Pro Lys
 305 310 315 320

Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser Asn Ile Phe Lys
 325 330 335

Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val Arg Arg Val Phe
 340 345 350

Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr Gln Trp Val Pro
 355 360 365

Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys
 370 375 380

Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro Asp Asp Val Ile
 385 390 395 400

Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro Val Phe Pro Met
 405 410 415

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Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly Gln Tyr Asp Val
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Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Val Ser Ile
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Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu Leu Glu Glu Met
 465 470 475 480

Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met Glu Leu Ser Thr
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Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly Val Ala Gln Leu
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Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys Ala Glu Cys Cys
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Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser Ala Cys Ser Arg
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Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln Asp Ile Arg Asn
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Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His Asp Asn His His
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Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val Glu Asn Ser Ser
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Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala Leu Val Tyr Trp
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Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu Ile Arg Val Asp
610 615 620

Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu Arg Ser Leu Gln
625 630 635 640

Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val Glu His Gly Phe
645 650 655

Ile Gln Thr Leu Leu Lys Val Thr Leu Glu Val Ile Asp Thr Glu His
660 665 670

Leu Glu Glu Leu Leu His Lys Asp Asp Asp Gly Asp Gly Ser Lys Thr
675 680 685

Lys Glu Met Ser Asn Ser Met Thr Pro Ser Gln Lys Val Trp Tyr Arg
690 695 700

Asp Phe Met Gln Leu Ile Asn His Pro Asn Leu Asn Thr Met Asp Glu
705 710 715 720

Phe Cys Glu Gln Val Trp Lys Arg Asp Arg Lys Gln Arg Arg Gln Arg
725 730 735

Pro Gly His Thr Pro Gly Asn Ser Asn Lys Trp Lys His Leu Gln Glu
740 745 750

Asn Lys Lys Gly Arg Asn Arg Arg Thr His Glu Phe Glu Arg Ala Pro
755 760 765

Arg Ser Val
770

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Met	Gly	Arg	Asp	Phe	Thr	Ile	Phe	Arg	Ser	Leu	Gly	Gln	Arg	Pro	Ser	
	195					200					205					
ctc	cga	aca	gag	cca	cac	gac	tcc	cgc	tgg	ctc	aat	gag	ccc	aag	ttt	910
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Val	Lys	Val	Phe	Trp	Ile	Pro	Glu	Ser	Glu	Asn	Pro	Asp	Asp	Asp	Lys	
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Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Thr	Ala	Val	Glu	Ala	Ala	Pro	Ala	Leu	
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Gly	Arg	Leu	Ser	Val	Ser	Arg	Val	Gly	Gln	Ile	Cys	Arg	Asn	Asp	Val	
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Gly	Gly	Gln	Arg	Ser	Leu	Val	Asn	Lys	Trp	Thr	Thr	Phe	Leu	Lys	Ala	
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cgg	ctg	gtg	tgc	tgc	gtg	ccc	ggc	gtc	gag	ggc	gac	acc	cac	ttc	gat	1150
Arg	Leu	Val	Cys	Ser	Val	Pro	Gly	Val	Glu	Gly	Asp	Thr	His	Phe	Asp	
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cag	ctc	cag	gat	gtg	ttt	ctg	ttg	tcc	tgc	cgg	gac	cac	cgg	acc	ccg	1198
Gln	Leu	Gln	Asp	Val	Phe	Leu	Leu	Ser	Ser	Arg	Asp	His	Arg	Thr	Pro	
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ctg	ctc	tat	gcc	gtc	ttc	tcc	acg	tcc	agc	agc	atc	ttc	cag	ggc	tct	1246
Leu	Leu	Tyr	Ala	Val	Phe	Ser	Thr	Ser	Ser	Ser	Ile	Phe	Gln	Gly	Ser	
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gcg	gtg	tgc	gtg	tac	agc	atg	aac	gac	gtg	cgc	cgg	gcc	ttc	ttg	gga	1294
Ala	Val	Cys	Val	Tyr	Ser	Met	Asn	Asp	Val	Arg	Arg	Ala	Phe	Leu	Gly	
		340					345					350				
ccc	ttt	gca	cac	aag	gag	ggg	ccc	atg	cac	cag	tgg	gtg	tca	tac	cag	1342
Pro	Phe	Ala	His	Lys	Glu	Gly	Pro	Met	His	Gln	Trp	Val	Ser	Tyr	Gln	
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Gly	Arg	Val	Pro	Tyr	Pro	Arg	Pro	Gly	Met	Cys	Pro	Ser	Lys	Thr	Phe	
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ggc	acc	ttc	agt	tcc	acc	aag	gac	ttc	cca	gac	gat	gtc	atc	cag	ttt	1438
Gly	Thr	Phe	Ser	Ser	Thr	Lys	Asp	Phe	Pro	Asp	Asp	Val	Ile	Gln	Phe	
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gcg	cgg	aac	cac	ccc	ctc	atg	tac	aac	tct	gtc	ctg	ccc	act	ggg	ggg	1486
Ala	Arg	Asn	His	Pro	Leu	Met	Tyr	Asn	Ser	Val	Leu	Pro	Thr	Gly	Gly	
			405					410					415			
cgc	cct	ctt	ttc	cta	caa	gtt	gga	gcc	aat	tac	acc	ttc	act	caa	att	1534
Arg	Pro	Leu	Phe	Leu	Gln	Val	Gly	Ala	Asn	Tyr	Thr	Phe	Thr	Gln	Ile	
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 Gly Arg Leu Phe Val Gly Ala Glu Asn His Val Ala Ser Leu Asn Leu
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 Asp Asn Ile Ser Lys Arg Ala Lys Lys Leu Ala Trp Pro Ala Pro Val
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Glu Trp Arg Glu Glu Cys Asn Trp Ala Gly Lys Asp Ile Gly Thr Glu
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Cys Met Asn Phe Val Lys Leu Leu His Ala Tyr Asn Arg Thr His Leu
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Leu Ala Cys Gly Thr Gly Ala Phe His Pro Thr Cys Ala Phe Val Glu
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Val Gly His Arg Ala Glu Glu Pro Val Leu Arg Leu Asp Pro Gly Arg
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Ile Glu Asp Gly Lys Gly Lys Ser Pro Tyr Asp Pro Arg His Arg Ala
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Ala Ser Val Leu Val Gly Glu Glu Leu Tyr Ser Gly Val Ala Ala Asp
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Leu Met Gly Arg Asp Phe Thr Ile Phe Arg Ser Leu Gly Gln Arg Pro
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Ser Leu Arg Thr Glu Pro His Asp Ser Arg Trp Leu Asn Glu Pro Lys
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Lys Ile Tyr Phe Phe Phe Arg Glu Thr Ala Val Glu Ala Ala Pro Ala
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Asp Gln Leu Gln Asp Val Phe Leu Leu Ser Ser Arg Asp His Arg Thr
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Pro Leu Leu Tyr Ala Val Phe Ser Thr Ser Ser Ser Ile Phe Gln Gly
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Ser Ala Val Cys Val Tyr Ser Met Asn Asp Val Arg Arg Ala Phe Leu
 340 345 350

Gly Pro Phe Ala His Lys Glu Gly Pro Met His Gln Trp Val Ser Tyr
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Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Met Cys Pro Ser Lys Thr
 370 375 380

Phe Gly Thr Phe Ser Ser Thr Lys Asp Phe Pro Asp Asp Val Ile Gln
 385 390 395 400

Phe Ala Arg Asn His Pro Leu Met Tyr Asn Ser Val Leu Pro Thr Gly
 405 410 415

Gly Arg Pro Leu Phe Leu Gln Val Gly Ala Asn Tyr Thr Phe Thr Gln
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Ile Ala Ala Asp Arg Val Ala Ala Ala Asp Gly His Tyr Asp Val Leu
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Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Ile Ser Val Pro
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Lys Gly Ser Arg Pro Ser Ala Glu Gly Leu Leu Leu Glu Glu Leu His
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Val Phe Glu Asp Ser Ala Ala Val Thr Ser Met Gln Ile Ser Ser Lys
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Arg Ala Glu Glu Ala Ala Pro Ala Ala Pro Pro Gly Pro Lys Leu Trp
675 680 685

Tyr Arg Asp Phe Leu Gln Leu Val Glu Pro Gly Gly Gly Gly Ser Ala
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Asn Ser Leu Arg Met Cys Arg Pro Gln Pro Ala Leu Gln Ser Leu Pro
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Trp Pro Ala Ser Thr Ile Lys Val Glu Glu Cys Lys Met Ala Gly Lys	
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His His Pro Leu Asp Tyr Arg Ile Leu Leu Met Asp Glu Asp Gln Asp
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Arg Ile Tyr Val Gly Ser Lys Asp His Ile Leu Ser Leu Asn Ile Asn
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Lys Val Glu Glu Cys Lys Met Ala Gly Lys Asp Pro Thr His Gly Cys
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Tyr Phe Phe Phe Lys Glu Lys Leu Thr Asp Asn Asn Arg Ser Thr Lys
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Gln Ile His Ser Met Ile Ala Arg Ile Cys Pro Asn Asp Thr Gly Gly
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Val Cys Ser Val Thr Asp Glu Asp Gly Pro Glu Thr His Phe Asp Glu
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Val Tyr Gly Ile Phe Thr Thr Ser Ser Ser Val Phe Lys Gly Ser Ala
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Phe Ala His Lys Glu Gly Pro Asn His Gln Leu Ile Ser Tyr Gln Gly
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Arg Ile Pro Tyr Pro Arg Pro Gly Thr Cys Pro Gly Gly Ala Phe Thr
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Pro Asn Met Arg Thr Thr Lys Glu Phe Pro Asp Asp Val Val Thr Phe
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Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile Tyr Pro Ile His Lys
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 Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr Lys Tyr Thr Lys Ile
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 Ala Val Asp Arg Val Asn Ala Ala Asp Gly Arg Tyr His Val Leu Phe
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 Lys Asn His Ala Pro Ile Thr Thr Met Lys Ile Ser Ser Lys Lys Gln
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 Lys Asp Arg Arg Lys Glu Val Lys Leu Asn Glu Arg Ile Ile Ala Thr
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 Tyr His Cys Ile Ala Thr Glu Asn Ser Phe Lys Gln Thr Ile Ala Lys
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Lys Trp Ser Pro Trp Thr Trp Ala Ser Ser Val Arg Ala Leu Pro Phe
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His Pro Lys Asp Ile Met Gly Ala Phe Ser His Ser Glu Met Gln Met
 690 695 700

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 Trp Thr Gly Gly His Thr Ala Asp Thr Thr His Pro Arg Leu Arg Leu
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 Gln Leu Leu Ala Gln Pro Glu Val Gly Leu Ile His Gln Tyr Cys Gln
 735 740 745

ggt tac tgg cgc cat gtg ccc ccc agc ccc agg gag gct cca ggg gca 2367
 Gly Tyr Trp Arg His Val Pro Pro Ser Pro Arg Glu Ala Pro Gly Ala
 750 755 760

ccc cgg tct cct gag ccc cag gac cag aaa aag ccc cgg aac cgc cgg 2415
 Pro Arg Ser Pro Glu Pro Gln Asp Gln Lys Lys Pro Arg Asn Arg Arg
 765 770 775

cac cac cct ccg gac aca tga ggccagctgc ctgtgcctgc catgggcccag 2466
 His His Pro Pro Asp Thr
 780 785

gctaggcctt ggccctttt aatataaaag atatatatat atatatatat atatattaaa 2526
 atatcgggggt ggggggtgat tggaaggag ggaggtggcc ttcccaatgc gcgttattcg 2586
 gggttattga agaataatat tgcaagtgc agccagaagt agactttctg tcctcacacc 2646
 gaagaaccgg agtgagcagg agggagggag agacgcgaag agaccttttt tcctttttgg 2706
 agaccttgtc cgc 2719

<210> 18
 <211> 785
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Leu Val Ala Gly Leu Leu Leu Trp Ala Ser Leu Leu Thr Gly Ala
 1 5 10 15

Trp Pro Ser Phe Pro Thr Gln Asp His Leu Pro Ala Thr Pro Arg Val
 20 25 30

Arg Leu Ser Phe Lys Glu Leu Lys Ala Thr Gly Thr Ala His Phe Phe
 35 40 45

Asn Phe Leu Leu Asn Thr Thr Asp Tyr Arg Ile Leu Leu Lys Asp Glu
 50 55 60

Asp His Asp Arg Met Tyr Val Gly Ser Lys Asp Tyr Val Leu Ser Leu
 65 70 75 80

Asp Leu His Asp Ile Asn Arg Glu Pro Leu Ile Ile His Trp Ala Ala
 85 90 95

Ser Pro Gln Arg Ile Glu Glu Cys Val Leu Ser Gly Lys Asp Val Asn
 100 105 110

Gly Glu Cys Gly Asn Phe Val Arg Leu Ile Gln Pro Trp Asn Arg Thr
 115 120 125

His Leu Tyr Val Cys Gly Thr Gly Ala Tyr Asn Pro Met Cys Thr Tyr
 130 135 140

Val Asn Arg Gly Arg Arg Ala Gln Ala Thr Pro Trp Thr Gln Thr Gln
 145 150 155 160

Ala Val Arg Gly Arg Gly Ser Arg Ala Thr Asp Gly Ala Leu Arg Pro
 165 170 175

Met Pro Thr Ala Pro Arg Gln Asp Tyr Ile Phe Tyr Leu Glu Pro Glu
 180 185 190

Arg Leu Glu Ser Gly Lys Gly Lys Cys Pro Tyr Asp Pro Lys Leu Asp
 195 200 205

Thr Ala Ser Ala Leu Ile Asn Glu Glu Leu Tyr Ala Gly Val Tyr Ile
 210 215 220

Asp Phe Met Gly Thr Asp Ala Ala Ile Phe Arg Thr Leu Gly Lys Gln
 225 230 235 240

Thr Ala Met Arg Thr Asp Gln Tyr Asn Ser Arg Trp Leu Asn Asp Pro
 245 250 255

Ser Phe Ile His Ala Glu Leu Ile Pro Asp Ser Ala Glu Arg Asn Asp
 260 265 270

Asp Lys Leu Tyr Phe Phe Phe Arg Glu Arg Ser Ala Glu Ala Pro Gln
 275 280 285

Ser Pro Ala Val Tyr Ala Arg Ile Gly Arg Ile Cys Leu Asn Asp Asp
 290 295 300

Gly Gly His Cys Cys Leu Val Asn Lys Trp Ser Thr Phe Leu Lys Ala
 305 310 315 320

Arg Leu Val Cys Ser Val Pro Gly Glu Asp Gly Ile Glu Thr His Phe
 325 330 335

Asp Glu Leu Gln Asp Val Phe Val Gln Gln Thr Gln Asp Val Arg Asn
 340 345 350

Pro Val Ile Tyr Ala Val Phe Thr Ser Ser Gly Ser Val Phe Arg Gly
 355 360 365

Ser Ala Val Cys Val Tyr Ser Met Ala Asp Ile Arg Met Val Phe Asn
 370 375 380

Gly Pro Phe Ala His Lys Glu Gly Pro Asn Tyr Gln Trp Met Pro Phe
 385 390 395 400

Ser Gly Lys Met Pro Tyr Pro Arg Pro Gly Thr Cys Pro Gly Gly Thr
 405 410 415

Phe Thr Pro Ser Met Lys Ser Thr Lys Asp Tyr Pro Asp Glu Val Ile
 420 425 430

Asn Phe Met Arg Ser His Pro Leu Met Tyr Gln Ala Val Tyr Pro Leu
 435 440 445

Gln Arg Arg Pro Leu Val Val Arg Thr Gly Ala Pro Tyr Arg Leu Thr
 450 455 460

Thr Ile Ala Val Asp Gln Val Asp Ala Gly Asp Gly Arg Tyr Glu Val
 465 470 475 480

Leu Phe Leu Gly Thr Asp Arg Gly Thr Val Gln Lys Val Ile Val Leu
 485 490 495

Pro Lys Asp Asp Gln Glu Met Glu Glu Leu Met Leu Glu Glu Val Glu
 500 505 510

Val Phe Lys Asp Pro Ala Pro Val Lys Thr Met Thr Ile Ser Ser Lys
 515 520 525

Arg Gln Gln Leu Tyr Val Ala Ser Ala Val Gly Val Thr His Leu Ser
 530 535 540

Leu His Arg Cys Gln Ala Tyr Gly Ala Ala Cys Ala Asp Cys Cys Leu
 545 550 555 560

Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Gln Ala Cys Ser Arg Tyr
 565 570 575

Thr Ala Ser Ser Lys Arg Arg Ser Arg Arg Gln Asp Val Arg His Gly
 580 585 590

Asn Pro Ile Arg Gln Cys Arg Gly Phe Asn Ser Asn Ala Asn Lys Asn
595 600 605

Ala Val Glu Ser Val Gln Tyr Gly Val Ala Gly Ser Ala Ala Phe Leu
610 615 620

Glu Cys Gln Pro Arg Ser Pro Gln Ala Thr Val Lys Trp Leu Phe Gln
625 630 635 640

Arg Asp Pro Gly Asp Arg Arg Arg Glu Ile Arg Ala Glu Asp Arg Phe
645 650 655

Leu Arg Thr Glu Gln Gly Leu Leu Leu Arg Ala Leu Gln Leu Ser Asp
660 665 670

Arg Gly Leu Tyr Ser Cys Thr Ala Thr Glu Asn Asn Phe Lys His Val
675 680 685

Val Thr Arg Val Gln Leu His Val Leu Gly Arg Asp Ala Val His Ala
690 695 700

Ala Leu Phe Pro Pro Leu Ser Met Ser Ala Pro Pro Pro Pro Gly Ala
705 710 715 720

Gly Pro Pro Thr Pro Pro Tyr Gln Glu Leu Ala Gln Leu Leu Ala Gln
725 730 735

Pro Glu Val Gly Leu Ile His Gln Tyr Cys Gln Gly Tyr Trp Arg His
740 745 750

Val Pro Pro Ser Pro Arg Glu Ala Pro Gly Ala Pro Arg Ser Pro Glu
755 760 765

Pro Gln Asp Gln Lys Lys Pro Arg Asn Arg Arg His His Pro Pro Asp
770 775 780

Thr
785

<210> 19
<211> 649
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (17)..(592)

<220>

<221> misc_feature

<222> (17)..(94)

<223> Signal peptide

<400> 19

tcgggcctcc gaaacc atg aac ttt ctg ctg tct tgg gtg cat tgg agc ctt	52
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu	
1 5 10	
gcc ttg ctg ctc tac ctc cac cat gcc aag tgg tcc cag gct gca ccc	100
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro	
15 20 25	
atg gca gaa gga gga ggg cag aat cat cac gaa gtg gtg aag ttc atg	148
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met	
30 35 40	
gat gtc tat cag cgc agc tac tgc cat cca atc gag acc ctg gtg gac	196
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp	
45 50 55 60	
atc ttc cag gag tac cct gat gag atc gag tac atc ttc aag cca tcc	244
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser	
65 70 75	
tgt gtg ccc ctg atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg	292
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
gag tgt gtg ccc act gag gag tcc aac atc acc atg cag att atg cgg	340
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
atc aaa cct cac caa ggc cag cac ata gga gag atg agc ttc cta cag	388
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
cac aac aaa tgt gaa tgc aga cca aag aaa gat aga gca aga caa gaa	436
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
aat ccc tgt ggg cct tgc tca gag cgg aga aag cat ttg ttt gta caa	484
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln	
145 150 155	
gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc	532
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys	
160 165 170	
aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt gac aag	580
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys	
175 180 185	
ccg agg cgg tga gccgggcagg aggaaggagc ctccctcagc gtttcgggaa	632
Pro Arg Arg	
190	
ccagatctct caccagg	649

<210> 20
 <211> 191
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (17)..(94)
 <223> Signal peptide

<400> 20

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160

Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
 165 170 175

Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
 180 185 190

<210> 21
 <211> 755
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (5)..(628)

<400> 21

cacc atg agc cct ctg ctc cgc cgc ctg ctg ctc gcc gca ctc ctg cag	49
Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln	
1 5 10 15	
ctg gcc ccc gcc cag gcc cct gtc tcc cag cct gat gcc cct ggc cac	97
Leu Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His	
20 25 30	
cag agg aaa gtg gtg tca tgg ata gat gtg tat act cgc gct acc tgc	145
Gln Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys	
35 40 45	
cag ccc cgg gag gtg gtg gtg ccc ttg act gtg gag ctc atg ggc acc	193
Gln Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr	
50 55 60	
gtg gcc aaa cag ctg gtg ccc agc tgc gtg act gtg cag cgc tgt ggt	241
Val Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly	
65 70 75	
ggc tgc tgc cct gac gat ggc ctg gag tgt gtg ccc act ggg cag cac	289
Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His	
80 85 90 95	
caa gtc cgg atg cag atc ctc atg atc cgg tac ccg agc agt cag ctg	337
Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu	
100 105 110	
ggg gag atg tcc ctg gaa gaa cac agc cag tgt gaa tgc aga cct aaa	385
Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys	
115 120 125	
aaa aag gac agt gct gtg aag cca gac agg gct gcc act ccc cac cac	433
Lys Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His	
130 135 140	
cgt ccc cag ccc cgt tct gtt ccg ggc tgg gac tct gcc ccc gga gca	481
Arg Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala	
145 150 155	
ccc tcc cca gct gac atc acc cat ccc act cca gcc cca ggc ccc tct	529
Pro Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser	
160 165 170 175	
gcc cac gct gca ccc agc acc acc agc gcc ctg acc ccc gga cct gcc	577
Ala His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala	
180 185 190	
gcc gcc gct gcc gac gcc gca gct tcc tcc gtt gcc aag ggc ggg gct	625
Ala Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala	
195 200 205	
tag agctcaaccc agacacctgc aggtgccgga agctgcgaag gtgacacatg	678
gcttttcaga ctcagcaggg tgacttgctt cagaggctat atcccagtgg gggaacaaaag	738

aggagcctgg taaaaaa

755

<210> 22
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 22

Met Ser Pro Leu Leu Arg Arg Leu Leu Leu Ala Ala Leu Leu Gln Leu
 1 5 10 15

Ala Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln
 20 25 30

Arg Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln
 35 40 45

Pro Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val
 50 55 60

Ala Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly
 65 70 75 80

Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln
 85 90 95

Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly
 100 105 110

Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys
 115 120 125

Lys Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg
 130 135 140

Pro Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro
 145 150 155 160

Ser Pro Ala Asp Ile Thr His Pro Thr Pro Ala Pro Gly Pro Ser Ala
 165 170 175

His Ala Ala Pro Ser Thr Thr Ser Ala Leu Thr Pro Gly Pro Ala Ala
 180 185 190

Ala Ala Ala Asp Ala Ala Ala Ser Ser Val Ala Lys Gly Gly Ala
 195 200 205

<210> 23
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (352)..(1611)

<400> 23
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 ctgcgtttcac ctgcggggct ccgaatgcgg ggagctcgga tgtccggttt cctgtgagggc 120
 ttttacctga caccgcgcgc ctttccccgg cactggctgg gagggcgccc tgcaaagttg 180
 ggaacgcgga gccccggacc cgtccccgcc gcctccggct cggccagggg gggtcgcccg 240
 gaggagccccg ggggagaggg accaggaggg gcccgcggcc tcgcaggggc gcccgcgccc 300
 ccacccctgc ccccgccagc ggaccgggtcc cccacccccg gtccttcac c atg cac 357
 Met His
 1
 ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
 Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
 5 10 15
 ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
 Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
 20 25 30
 gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
 Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
 35 40 45 50
 tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
 Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
 55 60 65
 gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
 Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
 70 75 80
 tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
 Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
 85 90 95
 ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
 Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
 100 105 110
 aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
 Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
 115 120 125 130
 tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
 Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
 135 140 145

gcg	aca	aac	acc	ttc	ttt	aaa	cct	cca	tgt	gtg	tcc	gtc	tac	aga	tgt	837
Ala	Thr	Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Ser	Val	Tyr	Arg	Cys	
		150						155				160				
ggg	ggt	tgc	tgc	aat	agt	gag	ggg	ctg	cag	tgc	atg	aac	acc	agc	acg	885
Gly	Gly	Cys	Cys	Asn	Ser	Glu	Gly	Leu	Gln	Cys	Met	Asn	Thr	Ser	Thr	
		165					170					175				
agc	tac	ctc	agc	aag	acg	tta	ttt	gaa	att	aca	gtg	cct	ctc	tct	caa	933
Ser	Tyr	Leu	Ser	Lys	Thr	Leu	Phe	Glu	Ile	Thr	Val	Pro	Leu	Ser	Gln	
	180					185					190					
ggc	ccc	aaa	cca	gta	aca	atc	agt	ttt	gcc	aat	cac	act	tcc	tgc	cga	981
Gly	Pro	Lys	Pro	Val	Thr	Ile	Ser	Phe	Ala	Asn	His	Thr	Ser	Cys	Arg	
195					200				205						210	
tgc	atg	tct	aaa	ctg	gat	gtt	tac	aga	caa	gtt	cat	tcc	att	att	aga	1029
Cys	Met	Ser	Lys	Leu	Asp	Val	Tyr	Arg	Gln	Val	His	Ser	Ile	Ile	Arg	
			215						220					225		
cgt	tcc	ctg	cca	gca	aca	cta	cca	cag	tgt	cag	gca	gcg	aac	aag	acc	1077
Arg	Ser	Leu	Pro	Ala	Thr	Leu	Pro	Gln	Cys	Gln	Ala	Ala	Asn	Lys	Thr	
			230					235					240			
tgc	ccc	acc	aat	tac	atg	tgg	aat	aat	cac	atc	tgc	aga	tgc	ctg	gct	1125
Cys	Pro	Thr	Asn	Tyr	Met	Trp	Asn	Asn	His	Ile	Cys	Arg	Cys	Leu	Ala	
		245					250					255				
cag	gaa	gat	ttt	atg	ttt	tcc	tgc	gat	gct	gga	gat	gac	tca	aca	gat	1173
Gln	Glu	Asp	Phe	Met	Phe	Ser	Ser	Asp	Ala	Gly	Asp	Asp	Ser	Thr	Asp	
	260					265					270					
gga	ttc	cat	gac	atc	tgt	gga	cca	aac	aag	gag	ctg	gat	gaa	gag	acc	1221
Gly	Phe	His	Asp	Ile	Cys	Gly	Pro	Asn	Lys	Glu	Leu	Asp	Glu	Glu	Thr	
275				280						285					290	
tgt	cag	tgt	gtc	tgc	aga	gcg	ggg	ctt	cgg	cct	gcc	agc	tgt	gga	ccc	1269
Cys	Gln	Cys	Val	Cys	Arg	Ala	Gly	Leu	Arg	Pro	Ala	Ser	Cys	Gly	Pro	
				295					300					305		
cac	aaa	gaa	cta	gac	aga	aac	tca	tgc	cag	tgt	gtc	tgt	aaa	aac	aaa	1317
His	Lys	Glu	Leu	Asp	Arg	Asn	Ser	Cys	Gln	Cys	Val	Cys	Lys	Asn	Lys	
		310						315					320			
ctc	ttc	ccc	agc	caa	tgt	ggg	gcc	aac	cga	gaa	ttt	gat	gaa	aac	aca	1365
Leu	Phe	Pro	Ser	Gln	Cys	Gly	Ala	Asn	Arg	Glu	Phe	Asp	Glu	Asn	Thr	
		325					330					335				
tgc	cag	tgt	gta	tgt	aaa	aga	acc	tgc	ccc	aga	aat	caa	ccc	cta	aat	1413
Cys	Gln	Cys	Val	Cys	Lys	Arg	Thr	Cys	Pro	Arg	Asn	Gln	Pro	Leu	Asn	
	340					345					350					
cct	gga	aaa	tgt	gcc	tgt	gaa	tgt	aca	gaa	agt	cca	cag	aaa	tgc	ttg	1461
Pro	Gly	Lys	Cys	Ala	Cys	Glu	Cys	Thr	Glu	Ser	Pro	Gln	Lys	Cys	Leu	
355					360					365					370	
tta	aaa	gga	aag	aag	ttc	cac	cac	caa	aca	tgc	agc	tgt	tac	aga	cgg	1509
Leu	Lys	Gly	Lys	Lys	Phe	His	His	Gln	Thr	Cys	Ser	Cys	Tyr	Arg	Arg	
				375					380					385		
cca	tgt	acg	aac	cgc	cag	aag	gct	tgt	gag	cca	gga	ttt	tca	tat	agt	1557
Pro	Cys	Thr	Asn	Arg	Gln	Lys	Ala	Cys	Glu	Pro	Gly	Phe	Ser	Tyr	Ser	
			390					395					400			

gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg 1605
 Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met
 405 410 415
 agc taa gattgtactg tttccagtt catcgatttt ctattatgga aaactgtgtt 1661
 Ser
 gccacagtag aactgtctgt gaacagagag acccttgtgg gtccatgcta acaaagacaa 1721
 aagtctgtct ttcctgaacc atgtggataa ctttacagaa atggactgga gctcatctgc 1781
 aaaaggcctc ttgtaaagac tggttttctg ccaatgacca aacagccaag attttcctct 1841
 tgtgatttct ttaaaagaat gactatataa tttatttcca ctaaaaatat tgtttctgca 1901
 ttcattttta tagcaacaac aattggtaaa actcactgtg atcaatattt ttatatcatg 1961
 caaaatatgt ttaaaataaa atgaaaattg tattat 1997

<210> 24
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 24

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
 1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
 20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
 35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
 50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
 65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
 85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
 100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
 115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
 130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
 405 410 415

Gln Met Ser

<210> 25
 <211> 2029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (411)..(1475)

<400> 25
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 aactagaacc tgcggcatac attggagaga tttttttaat tttctggaca tgaagtaaatt 120
 ttagagtgtt ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180
 cattttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240
 ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300
 tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360
 gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416
 Met Tyr
 1
 aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464
 Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
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 gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag 512
 Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
 20 25 30
 tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560
 Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
 35 40 45 50
 gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608
 Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
 55 60 65
 tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656
 Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
 70 75 80
 tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca 704
 Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
 85 90 95
 cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga 752
 Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
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 gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca 800
 Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
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Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys	
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Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser	
150 155 160	
aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta	944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
165 170 175	
gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg	1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	
aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta	1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt	1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
340 345 350	
tga ttcagcgttc caagttcccc atccctgtca tttttaacag catgctgctt	1525
tgccaagttg ctgtcactgt ttttttccca ggtgttaaaa aaaaaatcca ttttacacag	1585
caccacagtg aatccagacc aaccttccat tcacaccagc taaggagtcc ctggttcatt	1645

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<211> 354

<212> PRT

<213> Homo sapiens

<400> 26

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Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35 40 45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
 165 170 175

Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu
 180 185 190

Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
 195 200 205

Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile
 210 215 220

Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu
 225 230 235 240

Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala
 245 250 255

Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val
 260 265 270

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
 275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
 290 295 300

Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
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His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
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Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
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Asn Pro

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 <211> 1645
 <212> DNA
 <213> Homo sapiens

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 <222> (322)..(771)

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cccagccaca gccttaccta cgggctcctg actccgcaag gcttccagaa gatgctcgaa	180
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagcccccca ctcagctctt	240
ctcctcctgt gccaggggct ccccggggga tgagcatggt ggttttccct cggagccccc	300
tggtcgggga cgtctgagaa g atg ccg gtc atg agg ctg ttc cct tgc ttc Met Pro Val Met Arg Leu Phe Pro Cys Phe 1 5 10	351
ctg cag ctc ctg gcc ggg ctg gcg ctg cct gct gtg ccc ccc cag cag Leu Gln Leu Leu Ala Gly Leu Ala Leu Pro Ala Val Pro Pro Gln Gln 15 20 25	399
tgg gcc ttg tct gct ggg aac ggc tcg tca gag gtg gaa gtg gta ccc Trp Ala Leu Ser Ala Gly Asn Gly Ser Ser Glu Val Glu Val Val Pro 30 35 40	447
ttc cag gaa gtg tgg ggc cgc agc tac tgc cgg gcg ctg gag agg ctg Phe Gln Glu Val Trp Gly Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu 45 50 55	495
gtg gac gtc gtg tcc gag tac ccc agc gag gtg gag cac atg ttc agc Val Asp Val Val Ser Glu Tyr Pro Ser Glu Val Glu His Met Phe Ser 60 65 70	543
cca tcc tgt gtc tcc ctg ctg cgc tgc acc ggc tgc tgc ggc gat gag Pro Ser Cys Val Ser Leu Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu 75 80 85 90	591
aat ctg cac tgt gtg ccg gtg gag acg gcc aat gtc acc atg cag ctc Asn Leu His Cys Val Pro Val Glu Thr Ala Asn Val Thr Met Gln Leu 95 100 105	639
cta aag atc cgt tct ggg gac cgg ccc tcc tac gtg gag ctg acg ttc Leu Lys Ile Arg Ser Gly Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe 110 115 120	687
tct cag cac gtt cgc tgc gaa tgc cgg cct ctg cgg gag aag atg aag Ser Gln His Val Arg Cys Glu Cys Arg Pro Leu Arg Glu Lys Met Lys 125 130 135	735
ccg gaa agg tgc ggc gat gct gtt ccc cgg agg taa cccaccctt Pro Glu Arg Cys Gly Asp Ala Val Pro Arg Arg 140 145	781
ggaggagaga gacccccgac ccggctcgtg tatttattac cgtcacactc ttcagtgact	841
cctgctggta cctgccctct atttattagc caactgtttc cctgctgaat gcctcgctcc	901
cttcaagacg aggggcaggg aaggacagga ccctcaggaa ttcagtgcct tcaacaacgt	961
gagagaaaga gagaagccag ccacagaccc ctgggagctt ccgctttgaa agaagcaaga	1021
cacgtggcct cgtgaggggc aagctaggcc ccagaggccc tggaggctctc caggggcctg	1081
cagaaggaaa gaagggggcc ctgctacctg ttcttgggccc tcaggctctg cacagacaag	1141
cagcccttgc tttcggagct cctgtccaaa gtagggatgc ggattctgct ggggccgcca	1201

cggcctggtg gtgggaaggc cggcagcggg cggaggggat tcagccactt cccctcttct 1261
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 ccttggtccc cgtgatctcc cctcacactt tgccatttgc ttgtactggg acattgttct 1381
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 taaagtattc tagtgtggaa acgc 1645

<210> 28
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 <212> PRT
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 <400> 28

Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
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Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
 20 25 30

Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
 35 40 45

Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
 50 55 60

Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
 65 70 75 80

Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
 85 90 95

Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
 100 105 110

Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
 115 120 125

Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Cys Gly Asp
 130 135 140

Ala Val Pro Arg Arg
 145

<210> 29
 <211> 4230
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(4065)

<400> 29

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 Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu Thr Arg
 1 5 10 15

gcc gcc tct gtg ggt ttg cct agt gtt tct ctt gat ctg ccc agg ctc 96
 Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu
 20 25 30

agc ata caa aaa gac ata ctt aca att aag gct aat aca act ctt caa 144
 Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln
 35 40 45

att act tgc agg gga cag agg gac ttg gac tgg ctt tgg ccc aat aat 192
 Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn
 50 55 60

cag agt ggc agt gag caa agg gtg gag gtg act gag tgc agc gat ggc 240
 Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly
 65 70 75 80

ctc ttc tgt aag aca ctc aca att cca aaa gtg atc gga aat gac act 288
 Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn Asp Thr
 85 90 95

gga gcc tac aag tgc ttc tac cgg gaa act gac ttg gcc tcg gtc att 336
 Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser Val Ile
 100 105 110

tat gtc tat gtt caa gat tac aga tct cca ttt att gct tct gtt agt 384
 Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser
 115 120 125

gac caa cat gga gtc gtg tac att act gag aac aaa aac aaa act gtg 432
 Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val
 130 135 140

gtg att cca tgt ctc ggg tcc att tca aat ctc aac gtg tca ctt tgt 480
 Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys
 145 150 155 160

gca aga tac cca gaa aag aga ttt gtt cct gat ggt aac aga att tcc 528
 Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser
 165 170 175

tgg gac agc aag aag ggc ttt act att ccc agc tac atg atc agc tat 576
 Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr
 180 185 190

gct ggc atg gtc ttc tgt gaa gca aaa att aat gat gaa agt tac cag 624
 Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln
 195 200 205

tct att atg tac ata gtt gtc gtt gta ggg tat agg att tat gat gtg Ser Ile Met Tyr Ile Val Val Val Gly Tyr Arg Ile Tyr Asp Val 210 215 220	672
gtt ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag ctt Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu 225 230 235 240	720
gtc tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac ttc Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe 245 250 255	768
aac tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta aac Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn 260 265 270	816
cga gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg agc Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser 275 280 285	864
acc tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac acc Thr Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr 290 295 300	912
tgt gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt gtc Cys Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val 305 310 315 320	960
agg gtc cat gaa aaa cct ttt gtt gct ttt gga agt ggc atg gaa tct Arg Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser 325 330 335	1008
ctg gtg gaa gcc acg gtg ggg gag cgt gtc aga atc cct gcg aag tac Leu Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr 340 345 350	1056
ctt ggt tac cca ccc cca gaa ata aaa tgg tat aaa aat gga ata ccc Leu Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro 355 360 365	1104
ctt gag tcc aat cac aca att aaa gcg ggg cat gta ctg acg att atg Leu Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr Ile Met 370 375 380	1152
gaa gtg agt gaa aga gac aca gga aat tac act gtc atc ctt acc aat Glu Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu Thr Asn 385 390 395 400	1200
ccc att tca aag gag aag cag agc cat gtg gtc tct ctg gtt gtg tat Pro Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val Val Tyr 405 410 415	1248
gtc cca ccc cag att ggt gag aaa tct cta atc tct cct gtg gat tcc Val Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val Asp Ser 420 425 430	1296
tac cag tac ggc acc act caa acg ctg aca tgt acg gtc tat gcc att Tyr Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr Ala Ile 435 440 445	1344
cct ccc ccg cat cac atc cac tgg tat tgg cag ttg gag gaa gag tgc Pro Pro Pro His His Ile Trp Tyr Trp Gln Leu Glu Glu Glu Cys 450 455 460	1392

gcc aac gag ccc agc caa gct gtc tca gtg aca aac cca tac cct tgt Ala Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro Cys 465 470 475 480	1440
gaa gaa tgg aga agt gtg gag gac ttc cag gga gga aat aaa att gaa Glu Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu 485 490 495	1488
gtt aat aaa aat caa ttt gct cta att gaa gga aaa aac aaa act gta Val Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val 500 505 510	1536
agt acc ctt gtt atc caa gcg gca aat gtg tca gct ttg tac aaa tgt Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys 515 520 525	1584
gaa gcg gtc aac aaa gtc ggg aga gga gag agg gtg atc tcc ttc cac Glu Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser Phe His 530 535 540	1632
gtg acc agg ggt cct gaa att act ttg caa cct gac atg cag ccc act Val Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr 545 550 555 560	1680
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gag aac ctc aca tgg tac aag ctt ggc cca cag cct ctg cca atc cat Glu Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His 580 585 590	1776
gtg gga gag ttg ccc aca cct gtt tgc aag aac ttg gat act ctt tgg Val Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp 595 600 605	1824
aaa ttg aat gcc acc atg ttc tct aat agc aca aat gac att ttg atc Lys Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile 610 615 620	1872
atg gag ctt aag aat gca tcc ttg cag gac caa gga gac tat gtc tgc Met Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys 625 630 635 640	1920
ctt gct caa gac agg aag acc aag aaa aga cat tgc gtg gtc agg cag Leu Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val Arg Gln 645 650 655	1968
ctc aca gtc cta gag cgt gtg gca ccc acg atc aca gga aac ctg gag Leu Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn Leu Glu 660 665 670	2016
aat cag acg aca agt att ggg gaa agc atc gaa gtc tca tgc acg gca Asn Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys Thr Ala 675 680 685	2064
tct ggg aat ccc cct cca cag atc atg tgg ttt aaa gat aat gag acc Ser Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr 690 695 700	2112
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Thr Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr Cys Gln	
725 730 735	
gca tgc agt gtt ctt ggc tgt gca aaa gtg gag gca ttt ttc ata ata	2256
Ala Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe Ile Ile	
740 745 750	
gaa ggt gcc cag gaa aag acg aac ttg gaa atc att att cta gta ggc	2304
Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Ile Ile Ile Leu Val Gly	
755 760 765	
acg acg gtg att gcc atg ttc ttc tgg cta ctt ctt gtc atc atc cta	2352
Thr Thr Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Ile Leu	
770 775 780	
ggg acc gtt aag cgg gcc aat gga ggg gaa ctg aag aca ggc tac ttg	2400
Gly Thr Val Lys Arg Ala Asn Gly Gly Glu Leu Lys Thr Gly Tyr Leu	
785 790 795 800	
tcc atc gtc atg gat cca gat gaa ctc cca ttg gat gaa cat tgt gaa	2448
Ser Ile Val Met Asp Pro Asp Glu Leu Pro Leu Asp Glu His Cys Glu	
805 810 815	
cga ctg cct tat gat gcc agc aaa tgg gaa ttc ccc aga gac cgg ctg	2496
Arg Leu Pro Tyr Asp Ala Ser Lys Trp Glu Phe Pro Arg Asp Arg Leu	
820 825 830	
aac cta ggt aag cct ctt ggc cgt ggt gcc ttt ggc caa gag att gaa	2544
Asn Leu Gly Lys Pro Leu Gly Arg Gly Ala Phe Gly Gln Glu Ile Glu	
835 840 845	
gca gat gcc ttt gga att gac aag aca gca act tgc agg aca gta gca	2592
Ala Asp Ala Phe Gly Ile Asp Lys Thr Ala Thr Cys Arg Thr Val Ala	
850 855 860	
gtc aaa atg ttg aaa gaa gga gca aca cac agt gag cat cga gct ctc	2640
Val Lys Met Leu Lys Glu Gly Ala Thr His Ser Glu His Arg Ala Leu	
865 870 875 880	
atg tct gaa ctc aag atc ctc att cat att ggt cac cat ctc aat gtg	2688
Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly His His Leu Asn Val	
885 890 895	
gtc aac ctt cta ggt gcc tgt acc aag cca gga ggg cca ctc atg gtg	2736
Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gly Gly Pro Leu Met Val	
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Ile Val Glu Phe Cys Lys Phe Gly Asn Leu Ser Thr Tyr Leu Arg Ser	
915 920 925	
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Lys Arg Asn Glu Phe Val Pro Tyr Lys Thr Lys Gly Ala Arg Phe Arg	
930 935 940	
caa ggg aaa gac tac gtt gga gca atc cct gtg gat ctg aaa cgg cgc	2880
Gln Gly Lys Asp Tyr Val Gly Ala Ile Pro Val Asp Leu Lys Arg Arg	
945 950 955 960	
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Leu Asp Ser Ile Thr Ser Ser Gln Ser Ser Ala Ser Ser Gly Phe Val	
965 970 975	

gag gag aag tcc ctc agt gat gta gaa gaa gag gaa gct cct gaa gat	2976
Glu Glu Lys Ser Leu Ser Asp Val Glu Glu Glu Glu Ala Pro Glu Asp	
980 985 990	
ctg tat aag gac ttc ctg acc ttg gag cat ctc atc tgt tac agc ttc	3024
Leu Tyr Lys Asp Phe Leu Thr Leu Glu His Leu Ile Cys Tyr Ser Phe	
995 1000 1005	
caa gtg gct aag ggc atg gag ttc ttg gca tcg cga aag tgt atc	3069
Gln Val Ala Lys Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile	
1010 1015 1020	
cac agg gac ctg gcg gca cga aat atc ctc tta tcg gag aag aac	3114
His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Lys Asn	
1025 1030 1035	
gtg gtt aaa atc tgt gac ttt ggc ttg gcc cgg gat att tat aaa	3159
Val Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys	
1040 1045 1050	
gat cca gat tat gtc aga aaa gga gat gct cgc ctc cct ttg aaa	3204
Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala Arg Leu Pro Leu Lys	
1055 1060 1065	
tgg atg gcc cca gaa aca att ttt gac aga gtg tac aca atc cag	3249
Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val Tyr Thr Ile Gln	
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gag gaa gag gag gtc tgc atg gcc ccg cgc agc tct cag agc tca gaa 3604
 Glu Glu Glu Glu Val Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu
 1180 1185 1190 1195

gag ggc agc ttc tgc cag gtg tcc acc atg gcc cta cac atc gcc cag 3652
 Glu Gly Ser Phe Ser Gln Val Ser Thr Met Ala Leu His Ile Ala Gln
 1200 1205 1210

gct gac gct gag gac agc ccg cca agc ctg cag cgc cac agc ctg gcc 3700
 Ala Asp Ala Glu Asp Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala
 1215 1220 1225

gcc agg tat tac aac tgg gtg tcc ttt ccc ggg tgc ctg gcc aga ggg 3748
 Ala Arg Tyr Tyr Asn Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly
 1230 1235 1240

gct gag acc cgt ggt tcc tcc agg atg aag aca ttt gag gaa ttc ccc 3796
 Ala Glu Thr Arg Gly Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro
 1245 1250 1255

atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac agt 3844
 Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser
 1260 1265 1270 1275

ggg atg gtg ctg gcc tgc gag gag ttt gag cag ata gag agc agg cat 3892
 Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His
 1280 1285 1290

aga caa gaa agc ggc ttc agg tagctgaagc agagagagag aaggcagcat 3943
 Arg Gln Glu Ser Gly Phe Arg
 1295

acgtcagcat tttcttctct gcacttataa gaaagatcaa agactttaag actttcgcta 4003
 tttcttctac tgctatctac tacaaacttc aaagaggaac caggaggaca agaggagcat 4063
 gaaagtggac aaggagtgtg accactgaag caccacaggg aaggggttag gcctccggat 4123
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 tccctgactc ct 4195

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<211> 1298

<212> PRT

<213> Homo sapiens

<400> 32

Met Gln Arg Gly Ala Ala Leu Cys Leu Arg Leu Trp Leu Cys Leu Gly
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Leu Leu Asp Gly Leu Val Ser Gly Tyr Ser Met Thr Pro Pro Thr Leu
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Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser
 35 40 45

Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala
 50 55 60

Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val
 65 70 75 80

Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu
 85 90 95

Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr
 100 105 110

Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Ser
 115 120 125

Tyr Val Phe Val Arg Asp Phe Glu Gln Pro Phe Ile Asn Lys Pro Asp
 130 135 140

Thr Leu Leu Val Asn Arg Lys Asp Ala Met Trp Val Pro Cys Leu Val
 145 150 155 160

Ser Ile Pro Gly Leu Asn Val Thr Leu Arg Ser Gln Ser Ser Val Leu
 165 170 175

Trp Pro Asp Gly Gln Glu Val Val Trp Asp Asp Arg Arg Gly Met Leu
 180 185 190

Val Ser Thr Pro Leu Leu His Asp Ala Leu Tyr Leu Gln Cys Glu Thr
 195 200 205

Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn Pro Phe Leu Val His Ile
 210 215 220

Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Leu Pro Arg Lys Ser Leu
 225 230 235 240

Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn Cys Thr Val Trp Ala
 245 250 255

Glu Phe Asn Ser Gly Val Thr Phe Asp Trp Asp Tyr Pro Gly Lys Gln
 260 265 270

Ala Glu Arg Gly Lys Trp Val Pro Glu Arg Arg Ser Gln Gln Thr His
 275 280 285

Thr Glu Leu Ser Ser Ile Leu Thr Ile His Asn Val Ser Gln His Asp
 290 295 300

Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn Gly Ile Gln Arg Phe Arg
 305 310 315 320

Glu Ser Thr Glu Val Ile Val His Glu Asn Pro Phe Ile Ser Val Glu
 325 330 335

Trp Leu Lys Gly Pro Ile Leu Glu Ala Thr Ala Gly Asp Glu Leu Val
 340 345 350

Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro Pro Glu Phe Gln Trp
 355 360 365

Tyr Lys Asp Gly Lys Ala Leu Ser Gly Arg His Ser Pro His Ala Leu
 370 375 380

Val Leu Lys Glu Val Thr Glu Ala Ser Thr Gly Thr Tyr Thr Leu Ala
 385 390 395 400

Leu Trp Asn Ser Ala Ala Gly Leu Arg Arg Asn Ile Ser Leu Glu Leu
 405 410 415

Val Val Asn Val Pro Pro Gln Ile His Glu Lys Glu Ala Ser Ser Pro
 420 425 430

Ser Ile Tyr Ser Arg His Ser Arg Gln Ala Leu Thr Cys Thr Ala Tyr
 435 440 445

Gly Val Pro Leu Pro Leu Ser Ile Gln Trp His Trp Arg Pro Trp Thr
 450 455 460

Pro Cys Lys Met Phe Ala Gln Arg Ser Leu Arg Arg Arg Gln Gln Gln
 465 470 475 480

Asp Leu Met Pro Gln Cys Arg Asp Trp Arg Ala Val Thr Thr Gln Asp
 485 490 495

Ala Val Asn Pro Ile Glu Ser Leu Asp Thr Trp Thr Glu Phe Val Glu
 500 505 510

Gly Lys Asn Lys Thr Val Ser Lys Leu Val Ile Gln Asn Ala Asn Val
 515 520 525

Ser Ala Met Tyr Lys Cys Val Val Ser Asn Lys Val Gly Gln Asp Glu
 530 535 540

Arg Leu Ile Tyr Phe Tyr Val Thr Thr Ile Pro Asp Gly Phe Thr Ile
 545 550 555 560
 Glu Ser Lys Pro Ser Glu Glu Leu Leu Glu Gly Gln Pro Val Leu Leu
 565 570 575
 Ser Cys Gln Ala Asp Ser Tyr Lys Tyr Glu His Leu Arg Trp Tyr Arg
 580 585 590
 Leu Asn Leu Ser Thr Leu His Asp Ala His Gly Asn Pro Leu Leu Leu
 595 600 605
 Asp Cys Lys Asn Val His Leu Phe Ala Thr Pro Leu Ala Ala Ser Leu
 610 615 620
 Glu Glu Val Ala Pro Gly Ala Arg His Ala Thr Leu Ser Leu Ser Ile
 625 630 635 640
 Pro Arg Val Ala Pro Glu His Glu Gly His Tyr Val Cys Glu Val Gln
 645 650 655
 Asp Arg Arg Ser His Asp Lys His Cys His Lys Lys Tyr Leu Ser Val
 660 665 670
 Gln Ala Leu Glu Ala Pro Arg Leu Thr Gln Asn Leu Thr Asp Leu Leu
 675 680 685
 Val Asn Val Ser Asp Ser Leu Glu Met Gln Cys Leu Val Ala Gly Ala
 690 695 700
 His Ala Pro Ser Ile Val Trp Tyr Lys Asp Glu Arg Leu Leu Glu Glu
 705 710 715 720
 Lys Ser Gly Val Asp Leu Ala Asp Ser Asn Gln Lys Leu Ser Ile Gln
 725 730 735
 Arg Val Arg Glu Glu Asp Ala Gly Arg Tyr Leu Cys Ser Val Cys Asn
 740 745 750
 Ala Lys Gly Cys Val Asn Ser Ser Ala Ser Val Ala Val Glu Gly Ser
 755 760 765
 Glu Asp Lys Gly Ser Met Glu Ile Val Ile Leu Val Gly Thr Gly Val
 770 775 780
 Ile Ala Val Phe Phe Trp Val Leu Leu Leu Leu Ile Phe Cys Asn Met
 785 790 795 800

Arg Arg Pro Ala His Ala Asp Ile Lys Thr Gly Tyr Leu Ser Ile Ile
 805 810 815

Met Asp Pro Gly Glu Val Pro Leu Glu Glu Gln Cys Glu Tyr Leu Ser
 820 825 830

Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg Glu Arg Leu His Leu Gly
 835 840 845

Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys Val Val Glu Ala Ser Ala
 850 855 860

Phe Gly Ile His Lys Gly Ser Ser Cys Asp Thr Val Ala Val Lys Met
 865 870 875 880

Leu Lys Glu Gly Ala Thr Ala Ser Glu His Arg Ala Leu Met Ser Glu
 885 890 895

Leu Lys Ile Leu Ile His Ile Gly Asn His Leu Asn Val Val Asn Leu
 900 905 910

Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro Leu Met Val Ile Val Glu
 915 920 925

Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe Leu Arg Ala Lys Arg Asp
 930 935 940

Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro Glu Gln Arg Gly Arg Phe
 945 950 955 960

Arg Ala Met Val Glu Leu Ala Arg Leu Asp Arg Arg Arg Pro Gly Ser
 965 970 975

Ser Asp Arg Val Leu Phe Ala Arg Phe Ser Lys Thr Glu Gly Gly Ala
 980 985 990

Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu Asp Leu Trp Leu Ser Pro
 995 1000 1005

Leu Thr Met Glu Asp Leu Val Cys Tyr Ser Phe Gln Val Ala Arg Gly
 1010 1015 1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
 1025 1030 1035 1040

Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe

1045	1050	1055
Gly Leu Ala Arg 1060	Asp Ile Tyr Lys Asp 1065	Pro Asp Tyr Val Arg Lys Gly 1070
Ser Ala Arg 1075	Leu Pro Leu Lys Trp 1080	Met Ala Pro Glu Ser Ile Phe Asp 1085
Lys Val Tyr Thr Thr 1090	Gln Ser Asp Val Trp Ser Phe 1095	Gly Val Leu Leu 1100
Trp Glu Ile Phe Ser 1105	Leu Gly Ala Ser Pro Tyr 1110	Pro Gly Val Gln Ile 1115
Asn Glu Glu Phe Cys 1125	Gln Arg Leu Arg Asp 1130	Gly Thr Arg Met Arg Ala 1135
Pro Glu Leu Ala Thr 1140	Pro Ala Ile Arg Arg Ile Met Leu Asn Cys Trp 1145	1150
Ser Gly Asp 1155	Pro Lys Ala Arg Pro Ala Phe Ser Glu Leu Val Glu Ile 1160	1165
Leu Gly Asp Leu Leu Gln Gly 1170	Arg Gly Leu Gln Glu 1175	Glu Glu Glu Val 1180
Cys Met Ala Pro Arg Ser 1185	Ser Gln Ser Ser Glu 1190	Glu Gly Ser Phe Ser 1195
Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp 1205	1210	1215
Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn 1220	1225	1230
Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly 1235	1240	1245
Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr 1250	1255	1260
Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala 1265	1270	1275
Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly 1285	1290	1295

Phe Arg

<210> 33
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 33

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
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<210> 34
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 <213> Artificial sequence

<220>
 <223> Synthetic primer

<400> 34
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<210> 35
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<220>
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<400> 35
 aagttgggta acgccagg 18

<210> 36
 <211> 15
 <212> DNA
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<220>
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<400> 36
 tgacctcgcc cccgt 15

<210> 37
 <211> 3088
 <212> DNA
 <213> Homo sapiens

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tcatgttttt ttatacccg tttcccagct ccaatatgct gaagacctac ttctccgacg	2100
taaagttcaa cagatgcatt acctctcagc tcatcaagtg gtttagcaat ttccgtgagt	2160

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ctctacagac agtgatgtgt ctcttgtttc tactgctaag aaggtctgaa aatttaatga 2940
aaccacttca tacatttaag tattttgttt ggtttgaact caatcagtag cttttcctta 3000
catgtttaa aataattcca atgacagatg agcagctcac ttttccaaag taccceaaaa 3060
ggccaaatta aaaaaaaaaa aaaaaaaa 3088

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<210> 38

<211> 737

<212> PRT

<213> Homo sapiens

<400> 38

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Met Pro Asp His Asp Ser Thr Ala Leu Leu Ser Arg Gln Thr Lys Arg
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Arg Arg Val Asp Ile Gly Val Lys Arg Thr Val Gly Thr Ala Ser Ala
20           25           30

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Phe Phe Ala Lys Ala Arg Ala Thr Phe Phe Ser Ala Met Asn Pro Gln
35           40           45

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Gly Ser Glu Gln Asp Val Glu Tyr Ser Val Val Gln His Ala Asp Gly
50           55           60

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Glu Lys Ser Asn Val Leu Arg Lys Leu Leu Lys Arg Ala Asn Ser Tyr
65           70           75           80

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Glu Asp Ala Met Met Pro Phe Pro Gly Ala Thr Ile Ile Ser Gln Leu
85           90           95

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Leu Lys Asn Asn Met Asn Lys Asn Gly Gly Thr Glu Pro Ser Phe Gln
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 Ala Ser Gly Leu Ser Ser Thr Gly Ser Glu Val His Gln Glu Asp Ile
 115 120 125
 Cys Ser Asn Ser Ser Arg Asp Ser Pro Pro Glu Cys Leu Ser Pro Phe
 130 135 140
 Gly Arg Pro Thr Met Ser Gln Phe Asp Met Asp Arg Leu Cys Asp Glu
 145 150 155 160
 His Leu Arg Ala Lys Arg Ala Arg Val Glu Asn Ile Ile Arg Gly Met
 165 170 175
 Ser His Ser Pro Ser Val Ala Leu Arg Gly Asn Glu Asn Glu Arg Glu
 180 185 190
 Met Ala Pro Gln Ser Val Ser Pro Arg Glu Ser Tyr Arg Glu Asn Lys
 195 200 205
 Arg Lys Gln Lys Leu Pro Gln Gln Gln Gln Gln Ser Phe Gln Gln Leu
 210 215 220
 Val Ser Ala Arg Lys Glu Gln Lys Arg Glu Glu Arg Arg Gln Leu Lys
 225 230 235 240
 Gln Gln Leu Glu Asp Met Gln Lys Gln Leu Arg Gln Leu Gln Glu Lys
 245 250 255
 Phe Tyr Gln Ile Tyr Asp Ser Thr Asp Ser Glu Asn Asp Glu Asp Gly
 260 265 270
 Asn Leu Ser Glu Asp Ser Met Arg Ser Glu Ile Leu Asp Ala Arg Ala
 275 280 285
 Gln Asp Ser Val Gly Arg Ser Asp Asn Glu Met Cys Glu Leu Asp Pro
 290 295 300
 Gly Gln Phe Ile Asp Arg Ala Arg Ala Leu Ile Arg Glu Gln Glu Met
 305 310 315 320
 Ala Glu Asn Lys Pro Lys Arg Glu Gly Asn Asn Lys Glu Arg Asp His
 325 330 335
 Gly Pro Asn Ser Leu Gln Pro Glu Gly Lys His Leu Ala Glu Thr Leu
 340 345 350

Lys Gln Glu Leu Asn Thr Ala Met Ser Gln Val Val Asp Thr Val Val
355 360 365

Lys Val Phe Ser Ala Lys Pro Ser Arg Gln Val Pro Gln Val Phe Pro
370 375 380

Pro Leu Gln Ile Pro Gln Ala Arg Phe Ala Val Asn Gly Glu Asn His
385 390 395 400

Asn Phe His Thr Ala Asn Gln Arg Leu Gln Cys Phe Gly Asp Val Ile
405 410 415

Ile Pro Asn Pro Leu Asp Thr Phe Gly Asn Val Gln Met Ala Ser Ser
420 425 430

Thr Asp Gln Thr Glu Ala Leu Pro Leu Val Val Arg Lys Asn Ser Ser
435 440 445

Asp Gln Ser Ala Ser Gly Pro Ala Ala Gly Gly His His Gln Pro Leu
450 455 460

His Gln Ser Pro Leu Ser Ala Thr Thr Gly Phe Thr Thr Ser Thr Phe
465 470 475 480

Arg His Pro Phe Pro Leu Pro Leu Met Ala Tyr Pro Phe Gln Ser Pro
485 490 495

Leu Gly Ala Pro Ser Gly Ser Phe Ser Gly Lys Asp Arg Ala Ser Pro
500 505 510

Glu Ser Leu Asp Leu Thr Arg Asp Thr Thr Ser Leu Arg Thr Lys Met
515 520 525

Ser Ser His His Leu Ser His His Pro Cys Ser Pro Ala His Pro Pro
530 535 540

Ser Thr Ala Glu Gly Leu Ser Leu Ser Leu Ile Lys Ser Glu Cys Gly
545 550 555 560

Asp Leu Gln Asp Met Ser Glu Ile Ser Pro Tyr Ser Gly Ser Ala Met
565 570 575

Gln Glu Gly Leu Ser Pro Asn His Leu Lys Lys Ala Lys Leu Met Phe
580 585 590

Phe Tyr Thr Arg Tyr Pro Ser Ser Asn Met Leu Lys Thr Tyr Phe Ser
595 600 605

Asp Val Lys Phe Asn Arg Cys Ile Thr Ser Gln Leu Ile Lys Trp Phe
610 615 620

Ser Asn Phe Arg Glu Phe Tyr Tyr Ile Gln Met Glu Lys Tyr Ala Arg
625 630 635 640

Gln Ala Ile Asn Asp Gly Val Thr Ser Thr Glu Glu Leu Ser Ile Thr
645 650 655

Arg Asp Cys Glu Leu Tyr Arg Ala Leu Asn Met His Tyr Asn Lys Ala
660 665 670

Asn Asp Phe Glu Val Pro Glu Arg Phe Leu Glu Val Ala Gln Ile Thr
675 680 685

Leu Arg Glu Phe Phe Asn Ala Ile Ile Ala Gly Lys Asp Val Asp Pro
690 695 700

Ser Trp Lys Lys Ala Ile Tyr Lys Val Ile Cys Lys Leu Asp Ser Glu
705 710 715 720

Val Pro Glu Ile Phe Lys Ser Pro Asn Cys Leu Gln Glu Leu Leu His
725 730 735

Glu